

SEQUENCE LISTING

<110> Bachmann, Martin  
Vogt, Lorenz

<120> Immune Modulatory Compounds and Methods

<130> 1700.0390002

<150> 60/408,233  
<151> 2002-09-06

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Cys	Leu	Pro	Pro	Glu	Phe	Glu	Ala	Ile	Val	Trp	Asp	Ala	Gln	Asp	Leu	195	200	205	
Phe	Ser	Leu	Glu	Thr	Ser	Val	Val	Val	Arg	Ala	Gly	Ala	Leu	Ser	Asn	210	215	220	
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Val	Val	Gln	Ile	Ala	Asp	Val	Phe	Val	Pro	Gly	Ala	Ser	Ala	Trp	Lys	245	250	255	
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Pro Glu Tyr Pro Ile Leu Ala Leu Val Gly Glu Glu Val Glu Phe Pro 45 50 55

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Cys His Leu Trp Pro Gln Leu Asp Ala Gln Gln Met Glu Ile Arg Trp 60 65 70

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ggc acc atg cca gct acc aat gtc tct atc ttc att aat aac act cag Gly Thr Met Pro Ala Thr Asn Val Ser Ile Phe Ile Asn Asn Thr Gln 95 100 105 110			338
tta tca gac act ggc acc tac cag tgc ctg gtc aac aac ctt cca gac Leu Ser Asp Thr Gly Thr Tyr Gln Cys Leu Val Asn Asn Leu Pro Asp 115 120 125			386
ata ggg ggc agg aac att ggg gtc acc ggt ctc aca gtg tta gtt ccc Ile Gly Gly Arg Asn Ile Gly Val Thr Gly Leu Thr Val Leu Val Pro 130 135 140			434
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tac ctt tgg gag aag tta gac aat acc ctc aaa cta cct cca aca gct Tyr Leu Trp Glu Lys Leu Asp Asn Thr Leu Lys Leu Pro Pro Thr Ala 175 180 185 190			578
act cag gac cag gtc cag gga aca gtc acc atc cgg aac atc agt gcc Thr Gln Asp Gln Val Gln Gly Thr Val Thr Ile Arg Asn Ile Ser Ala 195 200 205			626
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agc acc tgt ctt ctg gat ctc cag gtt att tca ccc cag ccc agg aac Ser Thr Cys Leu Leu Asp Leu Gln Val Ile Ser Pro Gln Pro Arg Asn 225 230 235			722
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Val Ala Arg Gly Gln Thr Ala Val Leu Pro Cys Thr Phe Thr Thr Ser
              35              40              45

Ala Ala Leu Ile Asn Leu Asn Val Ile Trp Met Val Thr Pro Leu Ser
              50              55              60

Asn Ala Asn Gln Pro Glu Gln Val Ile Leu Tyr Gln Gly Gly Gln Met
65              70              75              80

Phe Asp Gly Ala Pro Arg Phe His Gly Arg Val Gly Phe Thr Gly Thr
              85              90              95

Met Pro Ala Thr Asn Val Ser Ile Phe Ile Asn Asn Thr Gln Leu Ser
              100              105              110

Asp Thr Gly Thr Tyr Gln Cys Leu Val Asn Asn Leu Pro Asp Ile Gly
              115              120              125

Gly Arg Asn Ile Gly Val Thr Gly Leu Thr Val Leu Val Pro Pro Ser
              130              135              140

Ala Pro His Cys Gln Ile Gln Gly Ser Gln Asp Ile Gly Ser Asp Val
145              150              155              160

Ile Leu Leu Cys Ser Ser Glu Glu Gly Ile Pro Arg Pro Thr Tyr Leu
              165              170              175

Trp Glu Lys Leu Asp Asn Thr Leu Lys Leu Pro Pro Thr Ala Thr Gln
              180              185              190

Asp Gln Val Gln Gly Thr Val Thr Ile Arg Asn Ile Ser Ala Leu Ser
              195              200              205

Ser Gly Leu Tyr Gln Cys Val Ala Ser Asn Ala Ile Gly Thr Ser Thr
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Met Thr Arg Arg Arg Ser Ala Pro Ala Ser Trp Leu Leu Val Ser  
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Leu Leu Gly Val Ala Thr Ser Leu Glu Val Ser Glu Ser Pro Gly Ser  
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gtc cag gtg gcc cgg ggc cag aca gca gtc ctg ccc tgc gcc ttc tcc 204  
Val Gln Val Ala Arg Gly Gln Thr Ala Val Leu Pro Cys Ala Phe Ser  
35 40 45  
acc agt gct gcc ctc ctg aac ctc aat gtc att tgg atg gtc att ccc 252  
Thr Ser Ala Ala Leu Leu Asn Leu Asn Val Ile Trp Met Val Ile Pro  
50 55 60  
ctc tcc aat gca aac cag ccc gaa cag gtc att ctt tat cag ggt gga 300  
Leu Ser Asn Ala Asn Gln Pro Glu Gln Val Ile Leu Tyr Gln Gly Gly  
65 70 75  
caa atg ttt gac ggc gcc ctc cgg ttc cac ggg agg gta gga ttt acc 348  
Gln Met Phe Asp Gly Ala Leu Arg Phe His Gly Arg Val Gly Phe Thr  
80 85 90 95  
ggc acc atg cct gct acc aat gtc tcg atc ttc atc aat aac aca cag 396  
Gly Thr Met Pro Ala Thr Asn Val Ser Ile Phe Ile Asn Asn Thr Gln  
100 105 110  
ctg tca gat acg ggc acg tac cag tgc ttg gtg aat aac ctt cca gac 444  
Leu Ser Asp Thr Gly Thr Tyr Gln Cys Leu Val Asn Asn Leu Pro Asp  
115 120 125  
aga ggg ggc aga aac atc ggg gtc act ggc ctc aca gtg tta gtc ccc 492  
Arg Gly Gly Arg Asn Ile Gly Val Thr Gly Leu Thr Val Leu Val Pro  
130 135 140  
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Pro Ser Ala Pro Gln Cys Gln Ile Gln Gly Ser Gln Asp Leu Gly Ser  
145 150 155  
gac gtc atc ctt ctg tgt agt tca gag gaa ggc atc cct cgg ccc acg 588

Asp	Val	Ile	Leu	Leu	Cys	Ser	Ser	Glu	Glu	Gly	Ile	Pro	Arg	Pro	Thr	
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Tyr	Leu	Trp	Glu	Lys	Leu	Asp	Asn	Thr	Leu	Lys	Leu	Pro	Pro	Thr	Ala	
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Thr	Gln	Asp	Gln	Val	Gln	Gly	Thr	Val	Thr	Ile	Arg	Asn	Ile	Ser	Ala	
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Leu	Ser	Ser	Gly	Leu	Tyr	Gln	Cys	Val	Ala	Ser	Asn	Ala	Ile	Gly	Thr	
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agc	acc	tgt	ctg	ctg	gac	ctc	cag	gtt	atc	tca	ccc	cag	ccc	cgg	agc	780
Ser	Thr	Cys	Leu	Leu	Asp	Leu	Gln	Val	Ile	Ser	Pro	Gln	Pro	Arg	Ser	
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Val	Gly	Val	Ile	Ala	Gly	Ala	Val	Gly	Thr	Gly	Ala	Val	Leu	Ile	Val	
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atc	tgc	ctt	gca	cta	att	tca	ggg	gcg	ttc	ttt	tac	tgg	aga	agc	aaa	876
Ile	Cys	Leu	Ala	Leu	Ile	Ser	Gly	Ala	Phe	Phe	Tyr	Trp	Arg	Ser	Lys	
			260					265						270		
aac	aaa	gag	gag	gag	gag	gaa	gaa	att	cct	aat	gaa	atc	aga	gag	gat	924
Asn	Lys	Glu	Glu	Glu	Glu	Glu	Glu	Ile	Pro	Asn	Glu	Ile	Arg	Glu	Asp	
		275						280					285			
gat	ctt	ccc	cct	aaa	tgc	tct	tct	gcc	aaa	gcc	ttc	cac	acg	gag	ata	972
Asp	Leu	Pro	Pro	Lys	Cys	Ser	Ser	Ala	Lys	Ala	Phe	His	Thr	Glu	Ile	
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Ser	Ser	Ser	Glu	Asn	Asn	Thr	Leu	Thr	Ser	Ser	Asn	Thr	Tyr	Asn	Ser	
	305					310					315					
cga	tac	tgg	aac	aac	aat	cca	aaa	ccc	cat	aga	aac	aca	gag	tct	ttc	1068
Arg	Tyr	Trp	Asn	Asn	Asn	Pro	Lys	Pro	His	Arg	Asn	Thr	Glu	Ser	Phe	
320				325				330							335	
aac	cac	ttc	agt	gac	tta	cgc	cag	tct	ttc	tct	ggc	aat	gca	gtt	atc	1116
Asn	His	Phe	Ser	Asp	Leu	Arg	Gln	Ser	Phe	Ser	Gly	Asn	Ala	Val	Ile	
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cca	tca	atc	tat	gca	aat	ggg	aac	cat	ctg	gtt	ttg	ggg	cca	cat	aag	1164
Pro	Ser	Ile	Tyr	Ala	Asn	Gly	Asn	His	Leu	Val	Leu	Gly	Pro	His	Lys	
		355					360					365				
act	ctg	gta	gtt	aca	gcc	aac	aga	ggg	tca	tca	cct	cag	gtc	ttg	ccc	1212
Thr	Leu	Val	Val	Thr	Ala	Asn	Arg	Gly	Ser	Ser	Pro	Gln	Val	Leu	Pro	
		370					375					380				
agg	aac	aat	ggg	tca	gtc	agc	agg	aag	cct	tgg	cct	caa	cac	act	cat	1260
Arg	Asn	Asn	Gly	Ser	Val	Ser	Arg	Lys	Pro	Trp	Pro	Gln	His	Thr	His	
	385					390					395					
tcc	tac	aca	gta	agc	caa	atg	acc	ctg	gag	cgc	atc	ggg	gca	gtg	cct	1308
Ser	Tyr	Thr	Val	Ser	Gln	Met	Thr	Leu	Glu	Arg	Ile	Gly	Ala	Val	Pro	
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35 40 45

Ser Ala Ala Leu Leu Asn Leu Asn Val Ile Trp Met Val Ile Pro Leu  
50 55 60

Ser Asn Ala Asn Gln Pro Glu Gln Val Ile Leu Tyr Gln Gly Gly Gln  
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Met Phe Asp Gly Ala Leu Arg Phe His Gly Arg Val Gly Phe Thr Gly  
85 90 95

Thr Met Pro Ala Thr Asn Val Ser Ile Phe Ile Asn Asn Thr Gln Leu  
100 105 110

Ser Asp Thr Gly Thr Tyr Gln Cys Leu Val Asn Asn Leu Pro Asp Arg  
115 120 125

Gly Gly Arg Asn Ile Gly Val Thr Gly Leu Thr Val Leu Val Pro Pro  
130 135 140

Ser Ala Pro Gln Cys Gln Ile Gln Gly Ser Gln Asp Leu Gly Ser Asp  
145 150 155 160

Val Ile Leu Leu Cys Ser Ser Glu Glu Gly Ile Pro Arg Pro Thr Tyr  
165 170 175

Leu Trp Glu Lys Leu Asp Asn Thr Leu Lys Leu Pro Pro Thr Ala Thr  
180 185 190

Gln Asp Gln Val Gln Gly Thr Val Thr Ile Arg Asn Ile Ser Ala Leu  
195 200 205

Ser Ser Gly Leu Tyr Gln Cys Val Ala Ser Asn Ala Ile Gly Thr Ser  
210 215 220

Thr Cys Leu Leu Asp Leu Gln Val Ile Ser Pro Gln Pro Arg Ser Val  
225 230 235 240

Gly Val Ile Ala Gly Ala Val Gly Thr Gly Ala Val Leu Ile Val Ile  
245 250 255

Cys Leu Ala Leu Ile Ser Gly Ala Phe Phe Tyr Trp Arg Ser Lys Asn  
260 265 270

Lys Glu Glu Glu Glu Glu Glu Ile Pro Asn Glu Ile Arg Glu Asp Asp  
275 280 285

Leu Pro Pro Lys Cys Ser Ser Ala Lys Ala Phe His Thr Glu Ile Ser  
290 295 300

Ser Ser Glu Asn Asn Thr Leu Thr Ser Ser Asn Thr Tyr Asn Ser Arg  
305 310 315 320

Tyr Trp Asn Asn Asn Pro Lys Pro His Arg Asn Thr Glu Ser Phe Asn  
325 330 335

His Phe Ser Asp Leu Arg Gln Ser Phe Ser Gly Asn Ala Val Ile Pro  
340 345 350

Ser Ile Tyr Ala Asn Gly Asn His Leu Val Leu Gly Pro His Lys Thr  
355 360 365

Leu Val Val Thr Ala Asn Arg Gly Ser Ser Pro Gln Val Leu Pro Arg  
370 375 380

Asn Asn Gly Ser Val Ser Arg Lys Pro Trp Pro Gln His Thr His Ser  
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Tyr Thr Val Ser Gln Met Thr Leu Glu Arg Ile Gly Ala Val Pro Val  
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<210> 11  
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<220>

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<222> (9)..(722)

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Ser Leu Leu Gly Val Ala Thr Ser Leu Glu Val Ser Glu Ser Pro Gly
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agt gtc cag gtg gcc cgg ggc cag aca gca gtc ctg ccc tgc gcc ttc      146
Ser Val Gln Val Ala Arg Gly Gln Thr Ala Val Leu Pro Cys Ala Phe
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tcc acc agt gct gcc ctc ctg aac ctc aat gtc att tgg atg gtc att      194
Ser Thr Ser Ala Ala Leu Leu Asn Leu Asn Val Ile Trp Met Val Ile
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ccc ctc tcc aat gca aac cag ccc gaa cag gtc att ctt tat cag ggt      242
Pro Leu Ser Asn Ala Asn Gln Pro Glu Gln Val Ile Leu Tyr Gln Gly
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gga caa atg ttt gac ggc gcc ctc cgg ttc cac ggg agg gta gga ttt      290
Gly Gln Met Phe Asp Gly Ala Leu Arg Phe His Gly Arg Val Gly Phe
      80              85              90

acc ggc acc atg cct gct acc aat gtc tcg atc ttc atc aat aac aca      338
Thr Gly Thr Met Pro Ala Thr Asn Val Ser Ile Phe Ile Asn Asn Thr
      95              100              105              110

cag ctg tca gat acg ggc acg tac cag tgc ttg gtg aat aac ctt cca      386
Gln Leu Ser Asp Thr Gly Thr Tyr Gln Cys Leu Val Asn Asn Leu Pro
              115              120              125

gac aga ggg ggc aga aac atc ggg gtc act ggc ctc aca gtg tta gtc      434
Asp Arg Gly Gly Arg Asn Ile Gly Val Thr Gly Leu Thr Val Leu Val
              130              135              140

ccc cct tct gct cca caa tgc caa atc caa gga tcc cag gac ctc ggc      482
Pro Pro Ser Ala Pro Gln Cys Gln Ile Gln Gly Ser Gln Asp Leu Gly
              145              150              155

agt gac gtc atc ctt ctg tgt agt tca gag gaa ggc atc cct cgg ccc      530
Ser Asp Val Ile Leu Leu Cys Ser Ser Glu Glu Gly Ile Pro Arg Pro
              160              165              170

acg tac ctt tgg gag aag tta gat aat acg ctc aag cta cct cca aca      578
Thr Tyr Leu Trp Glu Lys Leu Asp Asn Thr Leu Lys Leu Pro Pro Thr
      175              180              185              190

gcc act cag gac cag gtc cag gga aca gtc acc atc cgg aat atc agt      626
Ala Thr Gln Asp Gln Val Gln Gly Thr Val Thr Ile Arg Asn Ile Ser
              195              200              205

gcc ctc tct tcc ggt ctg tac cag tgt gtg gct tct aat gcc atc ggg      674

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Ala Leu Ser Ser Gly Leu Tyr Gln Cys Val Ala Ser Asn Ala Ile Gly  
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35 40 45

Ser Ala Ala Leu Leu Asn Leu Asn Val Ile Trp Met Val Ile Pro Leu  
50 55 60

Ser Asn Ala Asn Gln Pro Glu Gln Val Ile Leu Tyr Gln Gly Gly Gln  
65 70 75 80

Met Phe Asp Gly Ala Leu Arg Phe His Gly Arg Val Gly Phe Thr Gly  
85 90 95

Thr Met Pro Ala Thr Asn Val Ser Ile Phe Ile Asn Asn Thr Gln Leu  
100 105 110

Ser Asp Thr Gly Thr Tyr Gln Cys Leu Val Asn Asn Leu Pro Asp Arg  
115 120 125

Gly Gly Arg Asn Ile Gly Val Thr Gly Leu Thr Val Leu Val Pro Pro  
130 135 140

Ser Ala Pro Gln Cys Gln Ile Gln Gly Ser Gln Asp Leu Gly Ser Asp  
145 150 155 160

Val Ile Leu Leu Cys Ser Ser Glu Glu Gly Ile Pro Arg Pro Thr Tyr  
165 170 175

Leu Trp Glu Lys Leu Asp Asn Thr Leu Lys Leu Pro Pro Thr Ala Thr  
180 185 190

Gln Asp Gln Val Gln Gly Thr Val Thr Ile Arg Asn Ile Ser Ala Leu  
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Ser Ser Gly Leu Tyr Gln Cys Val Ala Ser Asn Ala Ile Gly Thr Ser  
210 215 220

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cta ata gtg ctc acc tat ggc cac ccc acc cta aaa aca cct gag agt 99  
Leu Ile Val Leu Thr Tyr Gly His Pro Thr Leu Lys Thr Pro Glu Ser  
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gtg aca ggg acc tgg aaa gga gat gtg aag att cag tgc atc tat gat 147  
Val Thr Gly Thr Trp Lys Gly Asp Val Lys Ile Gln Cys Ile Tyr Asp  
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ccc ctg aga ggc tac agg caa gtt ttg gtg aaa tgg ctg gta aga cac 195  
Pro Leu Arg Gly Tyr Arg Gln Val Leu Val Lys Trp Leu Val Arg His  
45 50 55 60

ggc tct gac tcc gtc acc atc ttc cta cgt gac tcc act gga gac cat 243  
Gly Ser Asp Ser Val Thr Ile Phe Leu Arg Asp Ser Thr Gly Asp His  
65 70 75

atc cag cag gca aag tac aga ggc cgc ctg aaa gtg agc cac aaa gtt 291  
Ile Gln Gln Ala Lys Tyr Arg Gly Arg Leu Lys Val Ser His Lys Val  
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Pro Gly Asp Val Ser Leu Gln Ile Asn Thr Leu Gln Met Asp Asp Arg  
95 100 105

aat cac tat aca tgt gag gtc acc tgg cag act cct gat gga aac caa 387  
Asn His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln  
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Val Ile Arg Asp Lys Ile Ile Glu Leu Arg Val Arg Lys Tyr Asn Pro  
125 130 135 140

cct aga atc aat act gaa gca cct aca acc ctg cac tcc tct ttg gaa 483  
Pro Arg Ile Asn Thr Glu Ala Pro Thr Thr Leu His Ser Ser Leu Glu  
145 150 155

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Ala Thr Thr Ile Met Ser Ser Thr Ser Asp Leu Thr Thr Asn Gly Thr  
160 165 170

gga aaa ctt gag gag acc att gct ggt tca ggg agg aac ctg cca atc 579  
Gly Lys Leu Glu Glu Thr Ile Ala Gly Ser Gly Arg Asn Leu Pro Ile  
175 180 185

ttt gcc ata atc ttc atc atc tcc ctt tgc tgc ata gta gct gtc acc 627  
Phe Ala Ile Ile Phe Ile Ile Ser Leu Cys Cys Ile Val Ala Val Thr  
190 195 200

ata cct tat atc ttg ttc cgc tgc agg aca ttc caa caa gag tat gtc 675  
Ile Pro Tyr Ile Leu Phe Arg Cys Arg Thr Phe Gln Gln Glu Tyr Val  
205 210 215 220

tat gga gtg agc agg gtg ttt gcc agg aag aca agc aac tct gaa gaa 723  
Tyr Gly Val Ser Arg Val Phe Ala Arg Lys Thr Ser Asn Ser Glu Glu  
225 230 235

acc aca agg gtg act acc atc gca act gat gaa cca gat tcc cag gct 771  
Thr Thr Arg Val Thr Thr Ile Ala Thr Asp Glu Pro Asp Ser Gln Ala  
240 245 250

ctg att agt gac tac tct gat gat cct tgc ctc agc cag gag tac caa 819  
Leu Ile Ser Asp Tyr Ser Asp Asp Pro Cys Leu Ser Gln Glu Tyr Gln  
255 260 265

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35 40 45

Tyr Arg Gln Val Leu Val Lys Trp Leu Val Arg His Gly Ser Asp Ser  
50 55 60

Val Thr Ile Phe Leu Arg Asp Ser Thr Gly Asp His Ile Gln Gln Ala  
65 70 75 80

Lys Tyr Arg Gly Arg Leu Lys Val Ser His Lys Val Pro Gly Asp Val  
85 90 95

Ser Leu Gln Ile Asn Thr Leu Gln Met Asp Asp Arg Asn His Tyr Thr  
100 105 110

Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Ile Arg Asp  
115 120 125

Lys Ile Ile Glu Leu Arg Val Arg Lys Tyr Asn Pro Pro Arg Ile Asn  
130 135 140

Thr Glu Ala Pro Thr Thr Leu His Ser Ser Leu Glu Ala Thr Thr Ile  
145 150 155 160

Met Ser Ser Thr Ser Asp Leu Thr Thr Asn Gly Thr Gly Lys Leu Glu  
165 170 175

Glu Thr Ile Ala Gly Ser Gly Arg Asn Leu Pro Ile Phe Ala Ile Ile  
180 185 190

Phe Ile Ile Ser Leu Cys Cys Ile Val Ala Val Thr Ile Pro Tyr Ile  
195 200 205

Leu Phe Arg Cys Arg Thr Phe Gln Gln Glu Tyr Val Tyr Gly Val Ser  
210 215 220

Arg Val Phe Ala Arg Lys Thr Ser Asn Ser Glu Glu Thr Thr Arg Val  
225 230 235 240

Thr Thr Ile Ala Thr Asp Glu Pro Asp Ser Gln Ala Leu Ile Ser Asp  
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260 265 270

Ser Thr Met Ser Ile Pro Ala Cys  
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Ile	Val	Leu	Thr	Tyr	Gly	His	Pro	Thr	Leu	Lys	Thr	Pro	Glu	Ser	Val	
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Thr	Gly	Thr	Trp	Lys	Gly	Asp	Val	Lys	Ile	Gln	Cys	Ile	Tyr	Asp	Pro	
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Leu	Arg	Gly	Tyr	Arg	Gln	Val	Leu	Val	Lys	Trp	Leu	Val	Arg	His	Gly	
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<220>
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<211> 20
<212> DNA
<213> Artificial Sequence

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<220>
<223> LV44-XM087714b primer

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<400> 26
ccacagcctt tagatgacgg 20

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<210> 27
<211> 27
<212> DNA
<213> Artificial Sequence

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<220>
<223> LV49-XM087714f primer

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<400> 27
gggggtacct gctgacgaga gatggtg 27

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<210> 28
<211> 25
<212> DNA
<213> Artificial Sequence

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<220>
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<400> 28

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<400> 30	
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<400> 33	
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<210> 34  
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<223> JS8-mB7-H5r primer

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23

<210> 35  
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<220>  
<223> MSt-1mB7-H5for primer

<400> 35  
ggggtaccat gactcggcgg cgctcc

26

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28

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<211> 21  
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<220>  
<223> LV80-mC18f

<400> 37  
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21

<210> 38  
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<220>  
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<210> 39  
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<223> LV82-mC18f primer

<400> 39
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<210> 40
<211> 23
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<220>
<223> LV83-mC18b primer

<400> 40
ggctagcagg ttcctccctg aac
23

<210> 41
<211> 1210
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (6)..(1202)

<400> 41
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1 5 10 15
50

gac act tat ggc cgt ccc atc ctg gaa gtg cca gag agt gta aca gga
Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr Gly
20 25 30
98

cct tgg aaa ggg gat gtg aat ctt ccc tgc acc tat gac ccc ctg caa
Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro Leu Gln
35 40 45
146

ggc tac acc caa gtc ttg gtg aag tgg ctg gta caa cgt ggc tca gac
Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp
50 55 60
194

cct gtc acc atc ttt cta cgt gac tct tct gga gac cat atc cag cag
Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln
65 70 75
242

gca aag tac cag ggc cgc ctg cat gtg agc cac aag gtt cca gga gat
Ala Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp
80 85 90 95
290

gta tcc ctc caa ttg agc acc ctg gag atg gat gac cgg agc cac tac
Val Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr
100 105 110
338

acg tgt gaa gtc acc tgg cag act cct gat ggc aac caa gtc gtg aga
386

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Thr	Cys	Glu	Val	Thr	Trp	Gln	Thr	Pro	Asp	Gly	Asn	Gln	Val	Val	Arg	
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gat	aag	att	act	gag	ctc	cgt	gtc	cag	aaa	ctc	tct	gtc	tcc	aag	ccc	434
Asp	Lys	Ile	Thr	Glu	Leu	Arg	Val	Gln	Lys	Leu	Ser	Val	Ser	Lys	Pro	
		130					135					140				
aca	gtg	aca	act	ggc	agc	ggc	tat	ggc	ttc	acg	gtg	ccc	cag	gga	atg	482
Thr	Val	Thr	Thr	Gly	Ser	Gly	Tyr	Gly	Phe	Thr	Val	Pro	Gln	Gly	Met	
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agg	att	agc	ctt	caa	tgc	cag	gct	cgg	ggc	tct	cct	ccc	atc	agt	tat	530
Arg	Ile	Ser	Leu	Gln	Cys	Gln	Ala	Arg	Gly	Ser	Pro	Pro	Ile	Ser	Tyr	
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Ile	Trp	Tyr	Lys	Gln	Gln	Thr	Asn	Asn	Gln	Glu	Pro	Ile	Lys	Val	Ala	
				180					185					190		
acc	cta	agt	acc	tta	ctc	ttc	aag	cct	gcg	gtg	ata	gcc	gac	tca	ggc	626
Thr	Leu	Ser	Thr	Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	
			195					200					205			
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Ser	Tyr	Phe	Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	
		210					215					220				
gac	att	gtg	aag	ttt	gtg	gtc	aaa	gac	tcc	tca	aag	cta	ctc	aag	acc	722
Asp	Ile	Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	
	225					230					235					
aag	act	gag	gca	cct	aca	acc	atg	aca	tac	ccc	ttg	aaa	gca	aca	tct	770
Lys	Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	
240					245					250					255	
aca	gtg	aag	cag	tcc	tgg	gac	tgg	acc	act	gac	atg	gat	ggc	tac	ctt	818
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	Leu	
				260					265					270		
gga	gag	acc	agt	gct	ggg	cca	gga	aag	agc	ctg	cct	gtc	ttt	gcc	atc	866
Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe	Ala	Ile	
			275					280					285			
atc	ctc	atc	atc	tcc	ttg	tgc	tgt	atg	gtg	gtt	ttt	acc	atg	gcc	tat	914
Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr	Met	Ala	Tyr	
		290					295					300				
atc	atg	ctc	tgt	cgg	aag	aca	tcc	caa	caa	gag	cat	gtc	tac	gaa	gca	962
Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His	Val	Tyr	Glu	Ala	
	305					310					315					
gcc	agg	gca	cat	gcc	aga	gag	gcc	aac	gac	tct	gga	gaa	acc	atg	agg	1010
Ala	Arg	Ala	His	Ala	Arg	Glu	Ala	Asn	Asp	Ser	Gly	Glu	Thr	Met	Arg	
320					325					330					335	
gtg	gcc	atc	ttc	gca	agt	ggc	tgc	tcc	agt	gat	gag	cca	act	tcc	cag	1058
Val	Ala	Ile	Phe	Ala	Ser	Gly	Cys	Ser	Ser	Asp	Glu	Pro	Thr	Ser	Gln	
				340					345					350		
aat	ctg	ggc	aac	aac	tac	tct	gat	gag	ccc	tgc	ata	gga	cag	gag	tac	1106
Asn	Leu	Gly	Asn	Asn	Tyr	Ser	Asp	Glu	Pro	Cys	Ile	Gly	Gln	Glu	Tyr	
			355					360					365			

cag atc atc gcc cag atc aat ggc aac tac gcc cgc ctg ctg gac aca 1154  
Gln Ile Ile Ala Gln Ile Asn Gly Asn Tyr Ala Arg Leu Leu Asp Thr  
370 375 380

gtt cct ctg gat tat gag ttt ctg gcc act gag ggc aaa agt gtc tgt 1202  
Val Pro Leu Asp Tyr Glu Phe Leu Ala Thr Glu Gly Lys Ser Val Cys  
385 390 395

taaaaatg 1210

<210> 42  
<211> 399  
<212> PRT  
<213> homo sapiens

<400> 42

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Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr Gly Pro  
20 25 30

Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro Leu Gln Gly  
35 40 45

Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp Pro  
50 55 60

Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln Ala  
65 70 75 80

Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp Val  
85 90 95

Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr Thr  
100 105 110

Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Val Arg Asp  
115 120 125

Lys Ile Thr Glu Leu Arg Val Gln Lys Leu Ser Val Ser Lys Pro Thr  
130 135 140

Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg  
145 150 155 160

Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile  
165 170 175

Trp Tyr Lys Gln Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr  
180 185 190

Leu Ser Thr Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser  
195 200 205

Tyr Phe Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp  
210 215 220

Ile Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys  
225 230 235 240

Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser Thr  
245 250 255

Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr Leu Gly  
260 265 270

Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe Ala Ile Ile  
275 280 285

Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr Met Ala Tyr Ile  
290 295 300

Met Leu Cys Arg Lys Thr Ser Gln Gln Glu His Val Tyr Glu Ala Ala  
305 310 315 320

Arg Ala His Ala Arg Glu Ala Asn Asp Ser Gly Glu Thr Met Arg Val  
325 330 335

Ala Ile Phe Ala Ser Gly Cys Ser Ser Asp Glu Pro Thr Ser Gln Asn  
340 345 350

Leu Gly Asn Asn Tyr Ser Asp Glu Pro Cys Ile Gly Gln Glu Tyr Gln  
355 360 365

Ile Ile Ala Gln Ile Asn Gly Asn Tyr Ala Arg Leu Leu Asp Thr Val  
370 375 380

Pro Leu Asp Tyr Glu Phe Leu Ala Thr Glu Gly Lys Ser Val Cys  
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<210> 43  
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<220>
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<222> (1)..(843)

<220>
<221> misc_feature
<222> (513)..(513)
<223> T at position 513 might be a C (silent mutation)

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Met Gly Ile Leu Leu Gly Leu Leu Leu Leu Gly His Leu Thr Val Asp
1          5          10          15

act tat ggc cgt ccc atc ctg gaa gtg cca gag agt gta aca gga cct      96
Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr Gly Pro
          20          25          30

tgg aaa ggg gat gtg aat ctt ccc tgc acc tat gac ccc ctg caa ggc      144
Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro Leu Gln Gly
          35          40          45

tac acc caa gtc ttg gtg aag tgg ctg gta caa cgt ggc tca gac cct      192
Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp Pro
          50          55          60

gtc acc atc ttt cta cgt gac tct tct gga gac cat atc cag cag gca      240
Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln Ala
65          70          75          80

aag tac cag ggc cgc ctg cat gtg agc cac aag gtt cca gga gat gta      288
Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp Val
          85          90          95

tcc ctc caa ttg agc acc ctg gag atg gat gac cgg agc cac tac acg      336
Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr Thr
          100          105          110

tgt gaa gtc acc tgg cag act cct gat ggc aac caa gtc gtg aga gat      384
Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Val Arg Asp
          115          120          125

aag att act gag ctc cgt gtc cag aaa ctc tct gtc tcc aag ccc aca      432
Lys Ile Thr Glu Leu Arg Val Gln Lys Leu Ser Val Ser Lys Pro Thr
          130          135          140

gtg aca act ggc agc ggt tat ggc ttc acg gtg ccc cag gga atg agg      480
Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg
145          150          155          160

att agc ctt caa tgc cag gct cgg ggt tct cct ccc atc agt tat att      528
Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile
          165          170          175

tgg tat aag caa cag act aat aac cag gaa ccc atc aaa gta gca acc      576
Trp Tyr Lys Gln Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr
          180          185          190

cta agt acc tta ctc ttc aag cct gcg gtg ata gcc gac tca ggc tcc      624
Leu Ser Thr Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser
          195          200          205

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tat	ttc	tgc	act	gcc	aag	ggc	cag	gtt	ggc	tct	gag	cag	cac	agc	gac	672
Tyr	Phe	Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	
	210					215					220					

att	gtg	aag	ttt	gtg	gtc	aaa	gac	tcc	tca	aag	cta	ctc	aag	acc	aag	720
Ile	Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys	
	225				230					235					240	

act	gag	gca	cct	aca	acc	atg	aca	tac	ccc	ttg	aaa	gca	aca	tct	aca	768
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	Thr	
			245						250					255		

gtg	aag	cag	tcc	tgg	gac	tgg	acc	act	gac	atg	gat	ggc	tac	ctt	gga	816
Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	Leu	Gly	
		260						265					270			

gag	acc	agt	gct	ggg	cca	gga	aag	cta	g							844
Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Leu								
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 <213> homo sapiens

<400> 44

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Trp	Lys	Gly	Asp	Val	Asn	Leu	Pro	Cys	Thr	Tyr	Asp	Pro	Leu	Gln	Gly
		35					40					45			

Tyr	Thr	Gln	Val	Leu	Val	Lys	Trp	Leu	Val	Gln	Arg	Gly	Ser	Asp	Pro
	50					55					60				

Val	Thr	Ile	Phe	Leu	Arg	Asp	Ser	Ser	Gly	Asp	His	Ile	Gln	Gln	Ala
65					70					75					80

Lys	Tyr	Gln	Gly	Arg	Leu	His	Val	Ser	His	Lys	Val	Pro	Gly	Asp	Val
				85					90					95	

Ser	Leu	Gln	Leu	Ser	Thr	Leu	Glu	Met	Asp	Asp	Arg	Ser	His	Tyr	Thr
			100					105					110		

Cys	Glu	Val	Thr	Trp	Gln	Thr	Pro	Asp	Gly	Asn	Gln	Val	Val	Arg	Asp
		115					120					125			

Lys	Ile	Thr	Glu	Leu	Arg	Val	Gln	Lys	Leu	Ser	Val	Ser	Lys	Pro	Thr
	130					135					140				

Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg  
145 150 155 160

Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile  
165 170 175

Trp Tyr Lys Gln Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr  
180 185 190

Leu Ser Thr Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser  
195 200 205

Tyr Phe Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp  
210 215 220

Ile Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys  
225 230 235 240

Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser Thr  
245 250 255

Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr Leu Gly  
260 265 270

Glu Thr Ser Ala Gly Pro Gly Lys Leu  
275 280

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<211> 10615  
<212> DNA  
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<220>  
<223> pCEP-hsB7-H6-COMP-FLAG

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